

FIG. 1

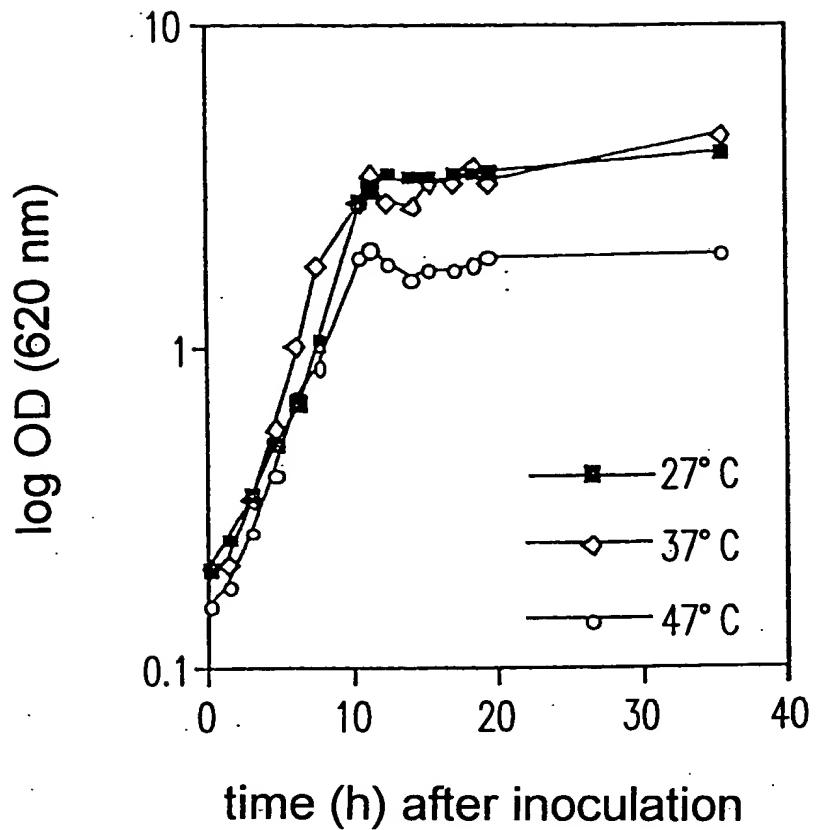
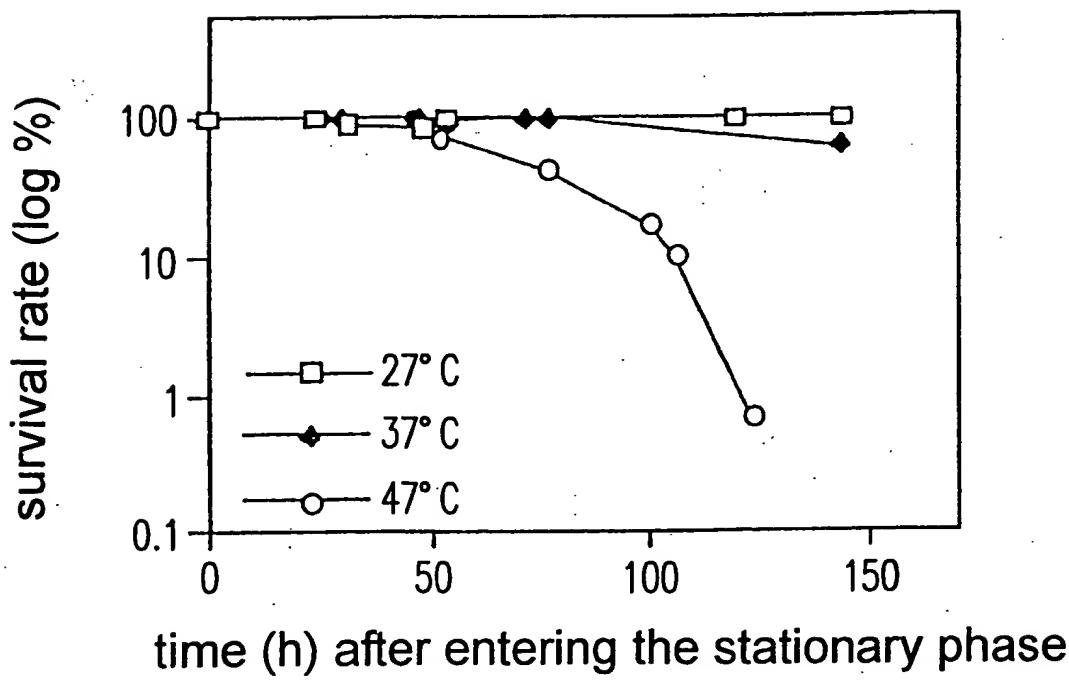


FIG. 2



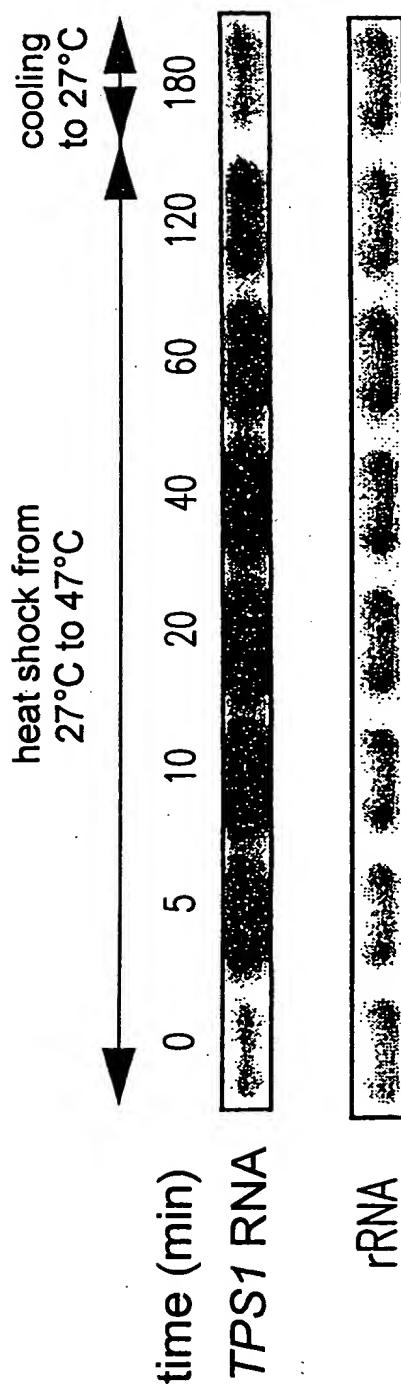


FIG. 3A

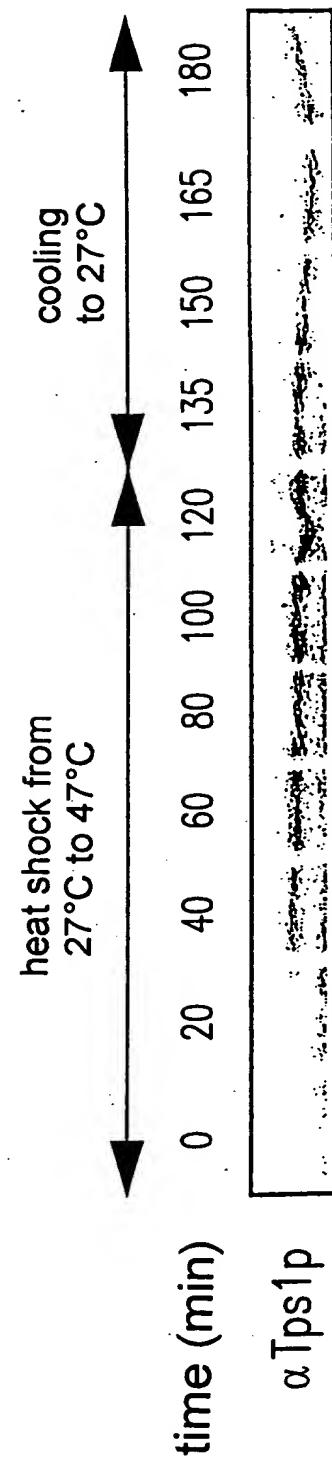


FIG. 3B

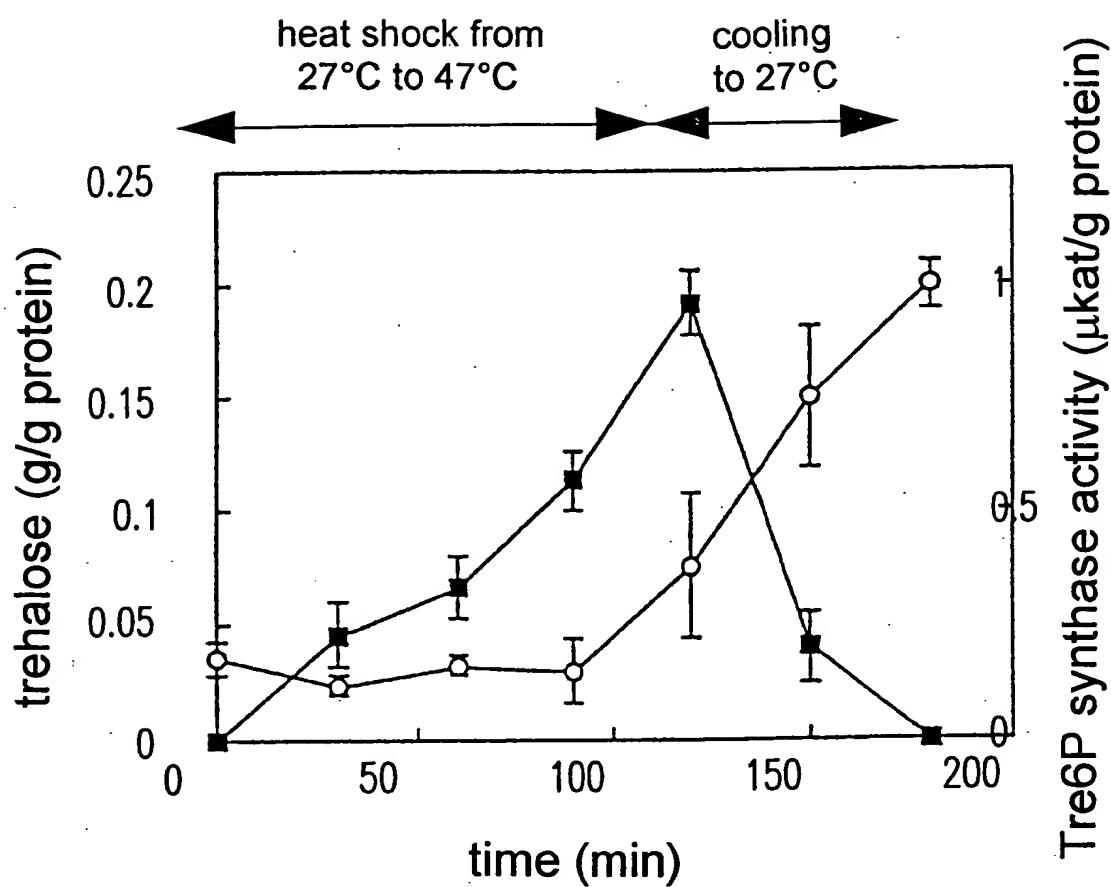
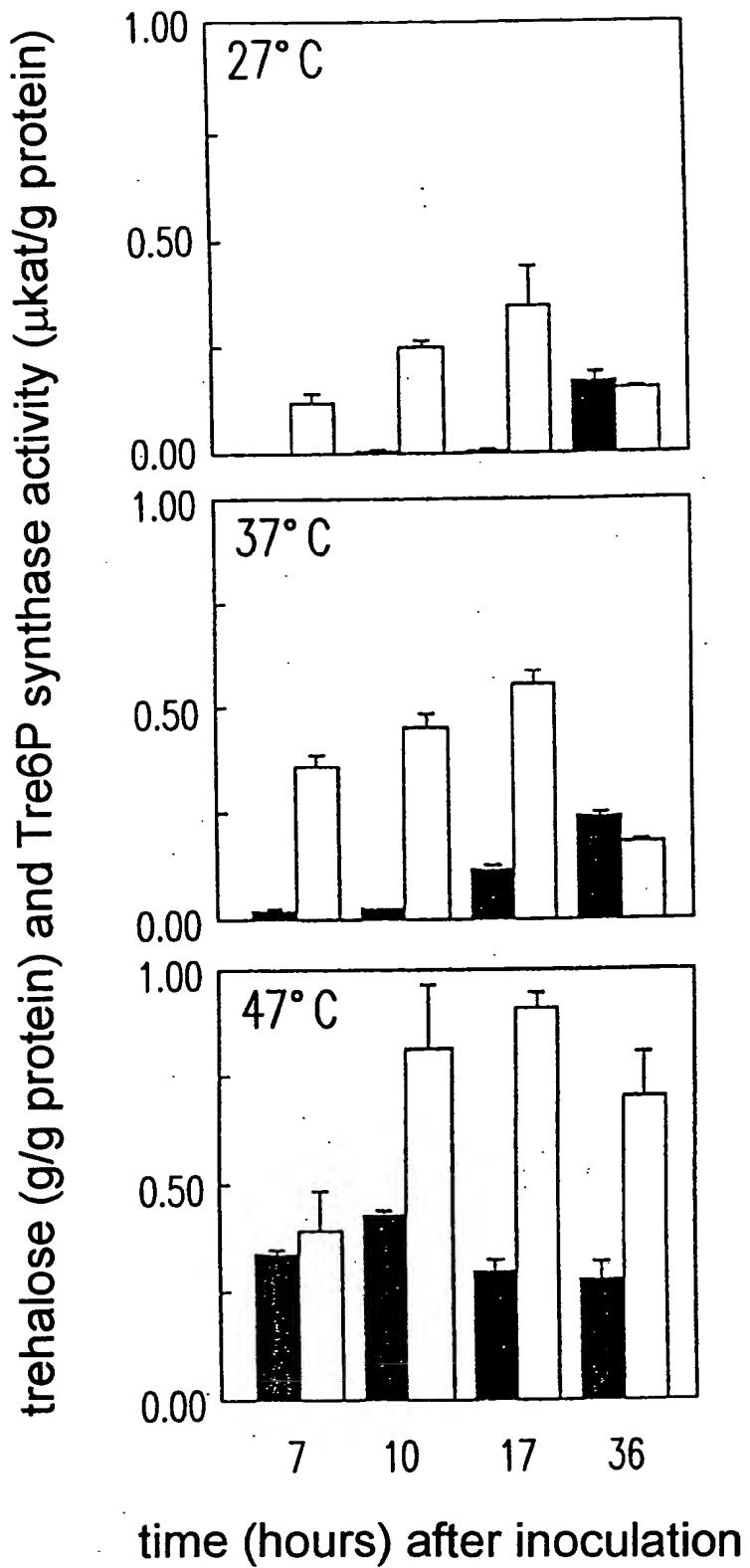


FIG. 3C

FIG. 4A



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FIG. 4B

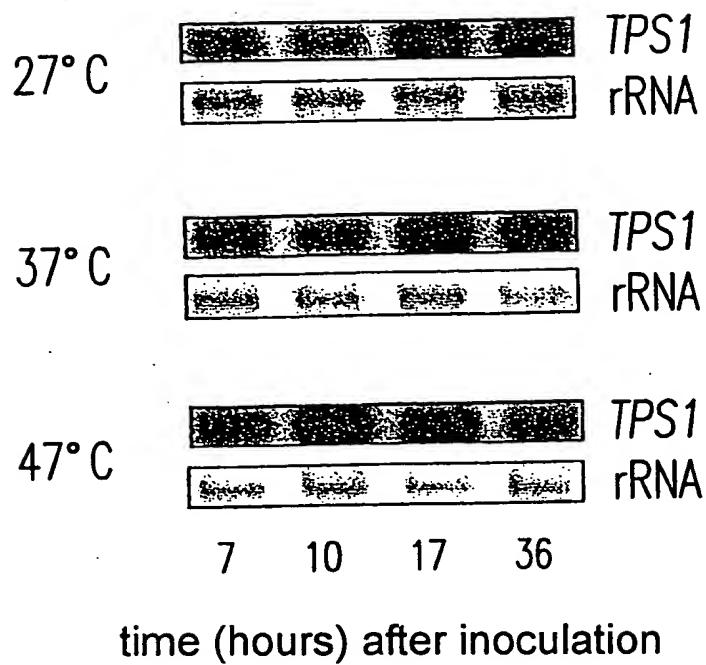
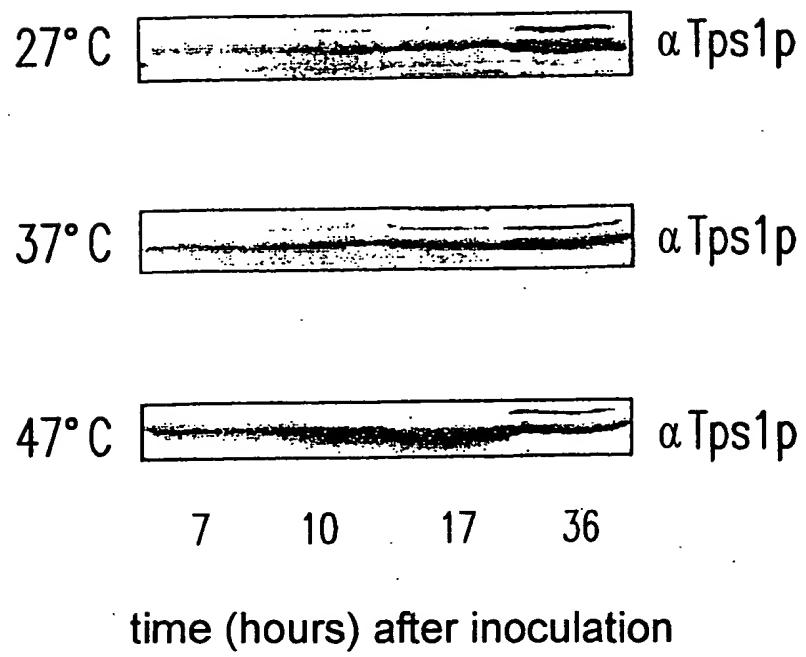


FIG. 4C



**TPS1 from**

*S. cerevisiae*  
*S. lactis*  
*S. alibicans*  
*S. pombe*  
*A. niger*

<b>1001</b> AGCGATGAAA TCGCAGACTT AC . TCTACAA CTGGTTCA GT AATTCTATTC ACTGACGAG TTGCTGTACTT TC ATTACAA CGGATTTCG AACCTCATTC AGTGAATACCA TTGCTGTATT AC ATTATAA TGGGTTTCG AATAGTATT GATGATGAGA CTCGCCGACCG CC ATTACAA CGGATTTAGT AACAGCATT CTGAGGGCC TTGCTTGCTG ACGGATATCC ACTGCTCAC AACTCCATT	<b>1050</b> AGTGCCTT ATTCCATTAC CATCCTTGG AGATCAATT CGACGAGAT TATGGCCATT GTTCCATTAC CATCCTTGG AGATCACTT CGATGACACT TATGGCCATT TTGCCATTAC CATCCTTGG AAATGAACTT TGATGAAAT TATGGCCATT GTTCCATTAC CATCCTTGG AAATTAACTT TCACCGAGGA TATGGCCATT GTTCCATTAC CATCCTTGG AGATTACCTT TGACCGAGTCC	<b>1100</b> GCGTGGTGG CATAACCGA GCGAACCCAG ACGTTACCA AGGAGATTC GCATCTTGC CGTACACCGA GGCAAATATG GCTTTGGCG ATGAAATTTGA GCGTGGCAG CATATATGA AGCCAAATAC AGTTTGCAT TGGAAATAGT CCTATGGAGG CCTATGGTGC GGCTAACTAC GCTTTGGCC AGCCCAATGT GCCTGGAAAG CATAACCGA GGCACACCGT CTTTCCCGA AGGGGTTC	<b>1150</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA	<b>1200</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA	<b>1250</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA	<b>1300</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA	<b>1350</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA	<b>1400</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA	<b>1450</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA	<b>1500</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA	<b>1550</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA	<b>1600</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA	<b>1650</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA	<b>1700</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA	<b>1750</b> GCGTGGCCTC AGAAGTTGCA AGAAGTTGCA GGTGTTCCCTC AGAAGTTACA GGTGTTCCCG AAAAATTACA GGTGTTCCC AAAAATTCCA GGTGTTCCCA AGAAGTTACA
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*S. cerevisiae*  
*S. lactis*  
*S. alibicans*  
*S. pombe*  
*A. niger*

**conserved regions**

*S. cerevisiae*  
*S. lactis*  
*S. alibicans*  
*S. pombe*  
*A. niger*

FIG. 5

## FIGUR 6

SEQ ID NO:8 (nucleic acid sequence)  
 SEQ ID NO:7 (amino acid sequence)

-792	CTTAAATACCACAATAGGAAAATTATCAATAAAGCTTTCTGGATTTCATTACGGTTATAATC	-733
-732	GCAAAAAAAATAGTCGAGCTTCTGAACCGTTCTGTAATAAAAAAAATAGTTTTTCAGATT	-673
-672	TCTATGTGAGGCAGTCACGATAGAATTCCATCGAACACTCGTCAGCGCCAAATGTGAATGCG	-613
-612	GCTTTCAAAGCTTGTGAATTGGATGGGAATCCATGAATCGAAGATGTCAAAATGG	-553
-552	GGGATCACAAAAGTACACTCACGAGGAAATCAAACCTCTCGTACCTTTAACACATAC	-493
-492	GGAAATGATCGATCGATTGAGAAGATTCTCAATGATTTCGTATATAGGTATCTG	-433
-432	AGGTATTATGGACCGATTCTGAATAACATCATACATCGGCTTGTCCCTGTCCCAG	-373
-372	AGATTTGATGAAAAAAGCGAATTTTATTCTAATAATTGAGCATGCCAAACATGGGCA	-313
-312	GTTGATTGTGTGAGGGTAAAATATCATGAATTGCACCCATCAAATGCAGCAAGATATTG	-253
-252	ACCAATCTATAATAGAAAACAGACTTACCCACAAATAGATTGTGATGACGATATTATGAA	-193
-192	TCTCCAGATGAAAGGCTGAAAGCTATGAAGCCCTTGTGAAACATTTCATGGTGAGATAAT	-133
-132	ATTTGAAATTTCACGAACTTCTAAACGCAATTATTGAAATATAAGGAAAAATAATA	-73
-72	TTTCCATATAGCAAGCAAATCAAGCTGACTCCTCATCCTAAACTAATAATCTTAC	-13
-12	CATTTGATACCAATGGTCAAAGGTAAATGTTATAGGGTTCAAATAGAATCCCAGTCACT	48
1	MetValLysGlyAsnValIleValValSerAsnArgIleProValThr	16
49	ATTAAGAAGACTGAAGATGATGAAAATGGAAAATCAAGATACGACTATACAATGTCATCA	108
17	IleLysLysThrGluAspAspGluAsnGlyLysSerArgTyrAspTyrThrMetSerSer	36
109	GGCGGATTAGTGACGGCATTACAAGGGCTCAAAAATCCATTTCGATGGTTGGATGGCCT	168
37	GlyGlyLeuValThrAlaLeuGlnGlyLeuLysAsnProPheArgTrpPheGlyTrpPro	56
169	GGGATGTCIGTTGATAGCGAACAGGGACGACAAACTGTCGAGCGGGATTGAAAGGAAAAG	228
57	GlyMetSerValAspSerGluGlnGlyArgGlnThrValGluArgAspLeuLysGluLys	76
229	TTCAATTGTTATCGATATGGTTAAGTGACGAAAATGCACTTACATTATAACGGCTTT	288
77	PheAsnCysTyrProIleTrpLeuSerAspGluIleAlaAspLeuHisTyrAsnGlyPhe	96
289	AGCAATTCTATACTTGGCCATTGTCACATACCCCCAGGGGAGATGAATTGATGAA	348
97	SerAsnSerIleLeuTrpProLeuPheHisTyrHisProGlyGluMetAsnPheAspGlu	116
349	ATTGCTGGGCCATTGGAAGCAAATAAACTGTTTGCCAAACGATCTTAAAGGAG	408
117	IleAlaTrpAlaAlaTyrLeuGluAlaAsnLysLeuPheCysGlnThrIleLeuLysGlu	136
409	ATAAAAGACGGGACGTTATCTGGGTACATGATTATCATCTCATGTTGTTGCCCTCACTG	468
137	IleLysAspGlyAspValIleTrpValHisAspTyrHisLeuMetLeuLeuProSerLeu	156
469	CTAAGAGACCAACTTAATAGTAAGGGCTACCGAATGTCAAAATTGGCTTTCCCTTCAT	528
157	LeuArgAspGlnLeuAsnSerLysGlyLeuProAsnValLysIleGlyPhePheLeuHis	176
529	ACTCCTTTCTCAAGCGAAATATACAGGATACTCCTGTAAGGAAAGAAATTCTCGAA	588
177	ThrProPheProSerSerGluIleTyrArgIleLeuProValArgLysGluIleLeuGlu	196
589	GGAGTGCTTAGTTGTGATTGATAGGGTTCCACACCTATGATTATGTCGTCACTTTCTT	648
197	GlyValLeuSerCysAspLeuIleGlyPheHisThrTyrAspTyrValArgHisPheLeu	216
649	AGTCGGTTGAAAGAATATGAAATTGCGAACGGAGCCCACAAGGTGTTGTCTATAATGAT	708
217	SerSerValGluArgIleLeuLysLeuArgThrSerProGlnGlyValValTyrAsnAsp	236

# FIGUR 6

(cont.)

709	AGACAGGTGACTGTAAGTGCTTATCOGATTGGCATTGACGTGACAAATTCTGAATGGT	768
237	ArgGlnValThrValSerAlaTyrProIleGlyIleAspValAspLysPheLeuAsnGly	256
769	CTTAAGACTGATGAGGTCAAAAGCAGGATAAAACAGCTGGAAACCAGATTGGTAAAGAT	828
257	LeuLysThrAspGluValLysSerArgIleLysGlnLeuGluThrArgPheGlyLysAsp	276
829	TGTAAACTTATTATTGGGTGGACAGGCTGGATTACATCAAAGGTGTACCTCAAAACTC	888
277	CysLysLeuIleIleGlyValAspArgLeuAspTyrIleLysGlyValProGlnLysLeu	296
889	CACGCCTTGAAATTTCCTGGAGAGACACCCCTGAGTGGATTGGAAAAGTTGTTTGATA	948
297	HisAlaPheGluIlePheLeuGluArgHisProGluTrpIleGlyLysValValLeuIle	316
949	CAGGTGGCTGTCCCCCTCACGAGGGGACGGTGAAGAATATCAATCTTGAGGGCAGCTGTA	1008
317	GlnValAlaValProSerArgGlyAspValGluGluTyrGlnSerLeuArgAlaAlaVal	336
1009	AATGAGCTAGTGGGAAGAACATCAATGGTAGATTGGTACCGTCGAATTGTTCCATATCCAT	1068
337	AsnGluLeuValGlyArgIleAsnGlyArgPheGlyThrValGluPheValProIleHis	356
1069	TTCCTTCATAAAAGCGTGAACCTCCAAGAGCTGATATCTGTCACGCTGCTAGTGATGTT	1128
357	PheLeuHisLysSerValAsnPheGlnGluLeuIleSerValTyrAlaAlaSerAspVal	376
1129	TGTGTAGTGTATCGACACGGGACGGAATGAATTGGTCAGITATGAATACTTGCTTGT	1188
377	CysValValSerSerThrArgAspGlyMetAsnLeuValSerTyrGluTyrIleAlaCys	396
1189	CAACAAAGATCGAAAGGGATCTCTAGTACTAAGTGAATTGGCGGGAGCTGCTCAGTCATTA	1248
397	GlnGlnAspArgLysGlySerLeuValLeuSerGluPheAlaGlyAlaAlaGlnSerLeu	416
1249	AATGGCGCTCTCGTAGTGAATCCATGGAATACAGAACGAACTCAGTGAAGCTATTACGAA	1308
417	AsnGlyAlaLeuValValAsnProTrpAsnThrGluGluLeuSerGluAlaIleTyrGlu	436
1309	GGCTTGATCATGAGTGAAGAGAAAAGGAGGGCAATTTCAGAAGATGTTCAAGTACATT	1368
437	GlyLeuIleMetSerGluGluLysArgArgGlyAsnPheGlnLysMetPheLysTyrIle	456
1369	GAGAAATATACTGCAAGTTATTGGGAGAGAACTTGTGAAAGAATTGACGAGAGTGTGA	1428
457	GluLysTyrThrAlaSerTyrTrpGlyGluAsnPheValLysGluLeuThrArgVal	476
1429	TTACTGTGGTTGCAAGGTTAATTGAAATGTTCACTTGTACTTGAAGAATTATATTAT	1488
1489	ATACATGTTATACATCAATAGGATAAAAATTAAAGTAGACAAAGTTATCATTTGTTGGC	1548
1549	TGTAAAAATTGAAACGATAACAATATATTGACAAAATTAAATTGATCTAATTGAGCTGGA	1608
1609	GGGCGTAATATATTGGTTCTGTAATCATCTTGTAGATCACAATATGGGGCAGCTTCTT	1668
1669	TCGCAGCCGATCACAGAGAACACATCACACTTGTCCAACATGATCACATATCGCATTCA	1728
1729	ATCGGGGAAATGCAAGGATACAGGTGACCATGGAAGACCGGTTCTGTGATTGAACGAA	1788
1789	AGAATATTGTCGTGACGGAAGAGGGACTTGACATCAGAAAACAAGACGAGAATACAGAGGT	1848
1849	GATCTGGAGTCTCTCAAATTAAACATTATGGTGTCTTGACGGACATGGCGGTT	1903

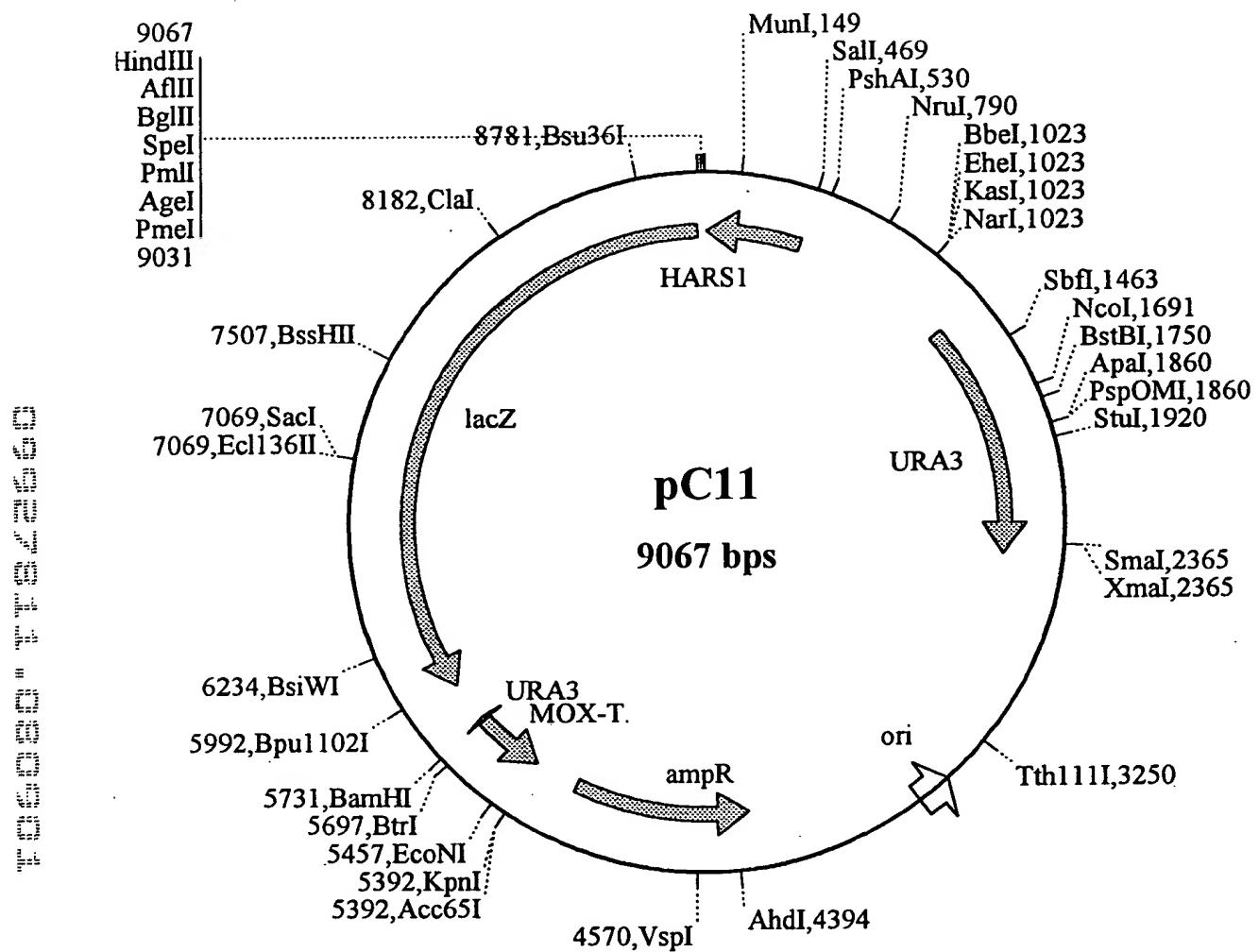


FIG. 7

0 999 888 777 666 555 444 333 222 111

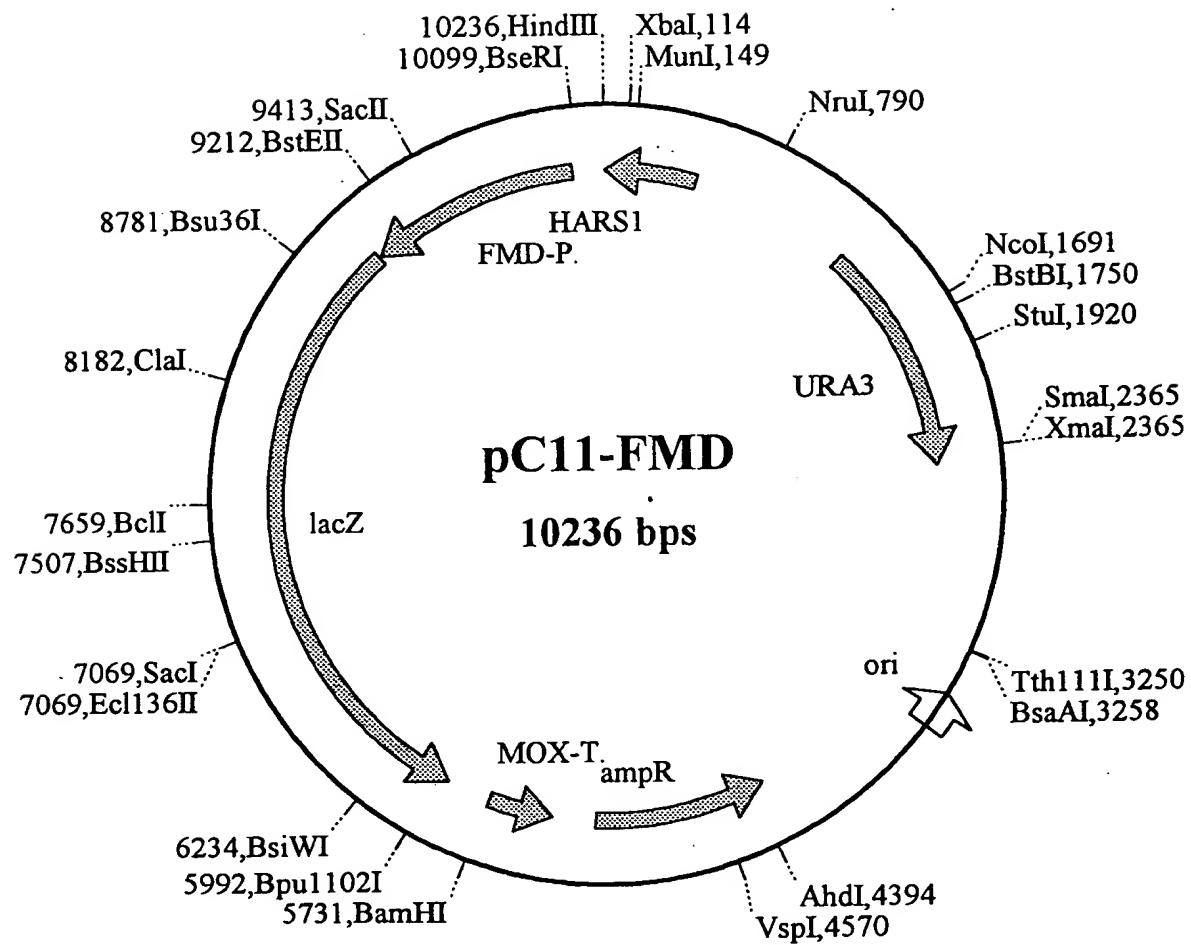


FIG. 8

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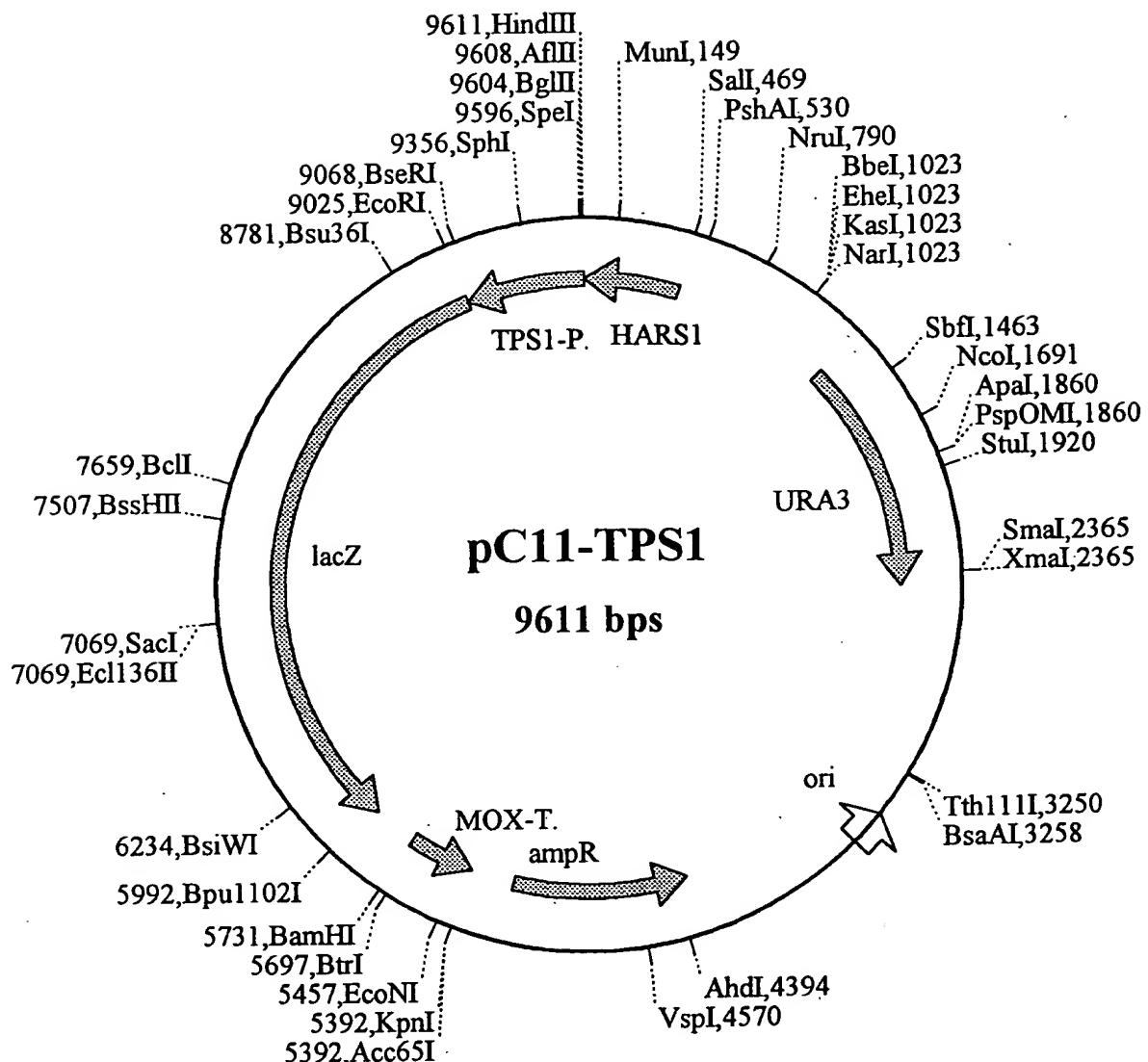


FIG. 9

FIG. 10A

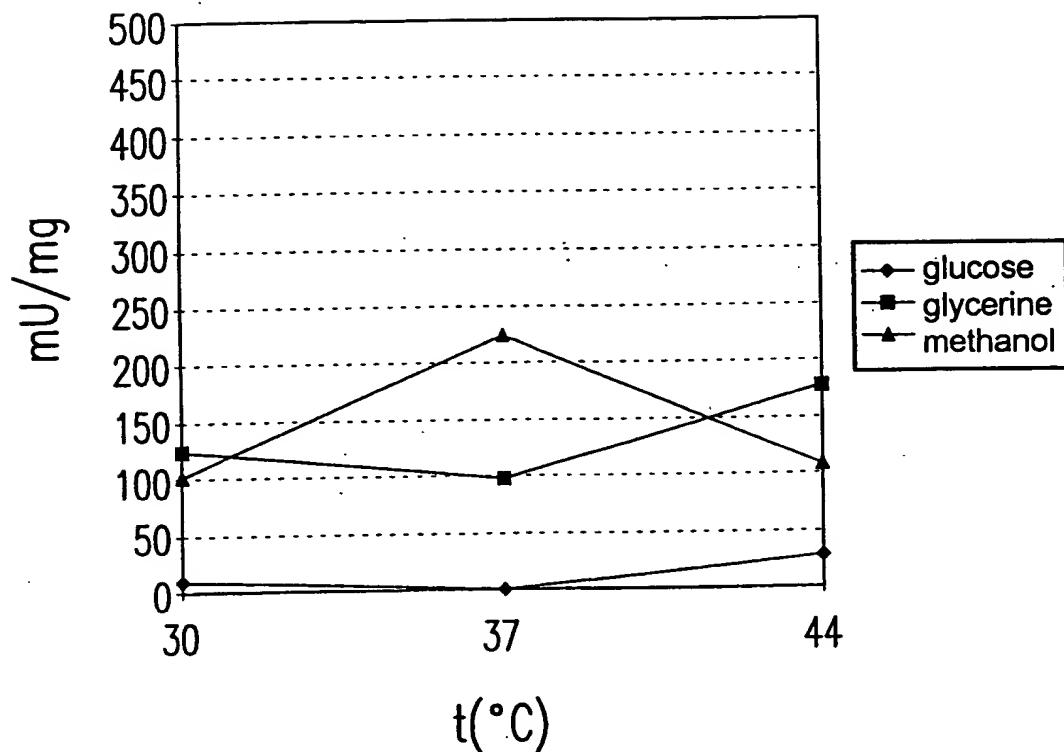
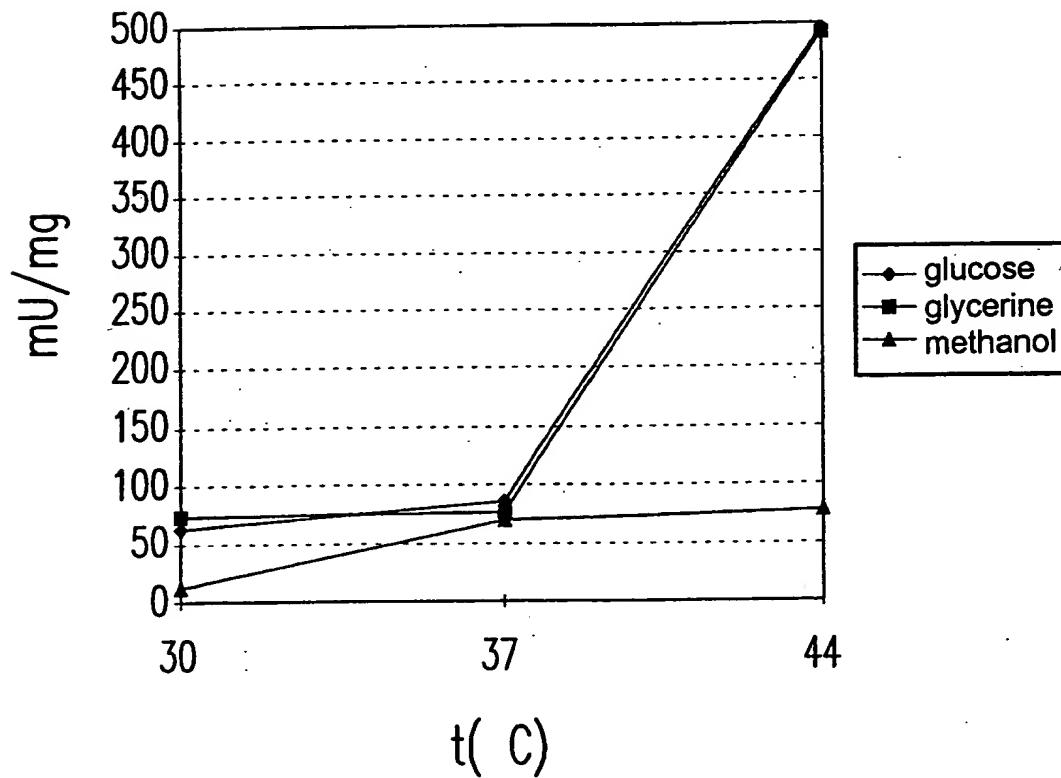


FIG. 10B



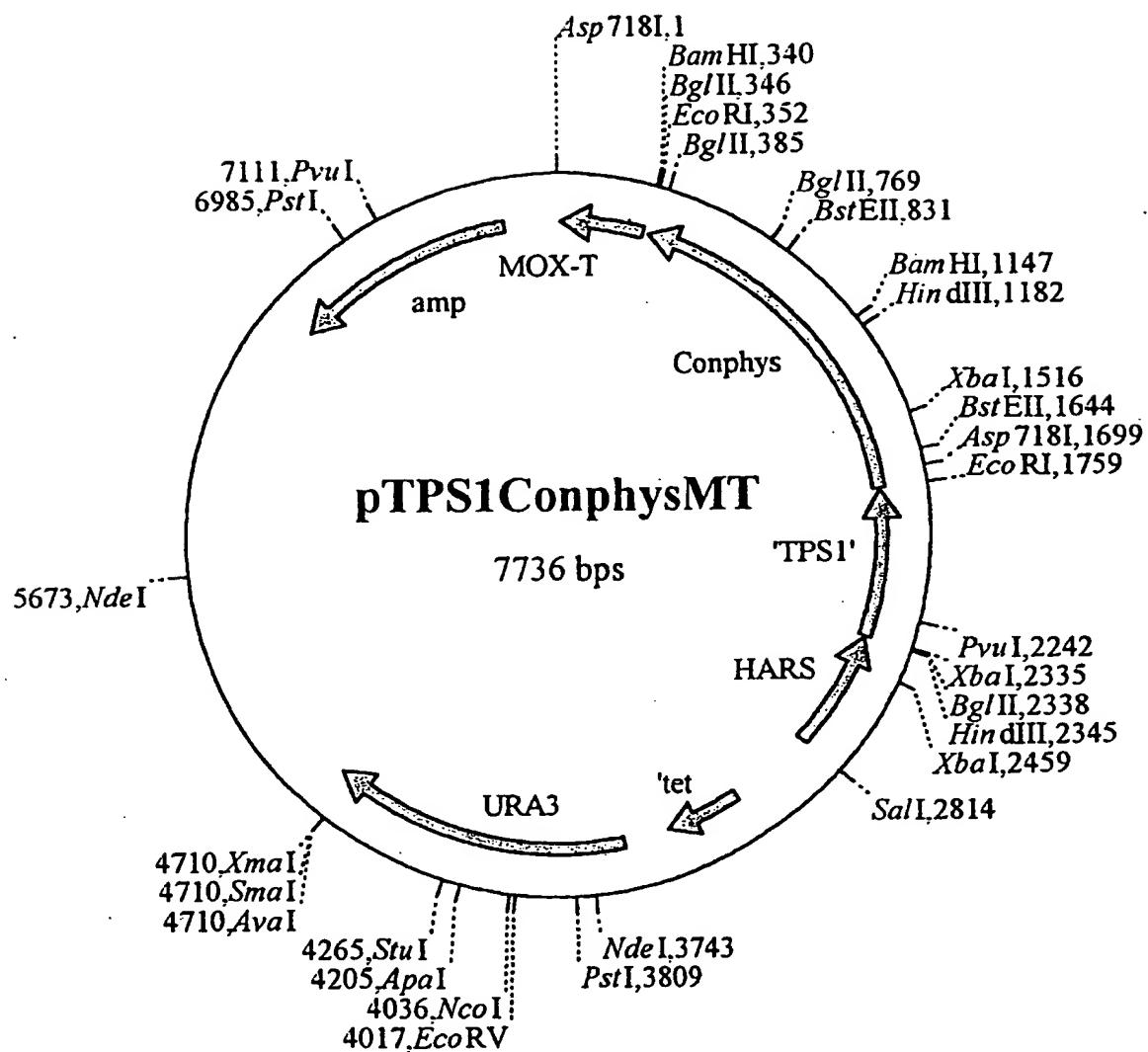


FIG. 11